



RAW SEQUENCE LISTING

DATE: 09/27/2002

PATENT APPLICATION: US/09/963,347B

TIME: 13:57:41

Input Set : A:\DX0903K1.ST25.txt

Output Set: N:\CRF4\09272002\I963347B.raw

```

3 <110> APPLICANT: Bazan, J. Fernando
4 de Waal Malefyt, Rene
5 Liu, Yong-Jun
6 Soumelis, Vassili
8 <120> TITLE OF INVENTION: MAMMALIAN CYTOKINES; RELATED REAGENTS AND METHODS
10 <130> FILE REFERENCE: DX0903K1
12 <140> CURRENT APPLICATION NUMBER: US 09/963,347B
13 <141> CURRENT FILING DATE: 2001-09-25
15 <150> PRIOR APPLICATION NUMBER: US 09/399,492
16 <151> PRIOR FILING DATE: 1999-09-20
18 <150> PRIOR APPLICATION NUMBER: US 60/131,298
19 <151> PRIOR FILING DATE: 1999-04-27
21 <150> PRIOR APPLICATION NUMBER: US 60/101,318
22 <151> PRIOR FILING DATE: 1998-09-21
24 <160> NUMBER OF SEQ ID NOS: 9
26 <170> SOFTWARE: PatentIn version 3.1
28 <210> SEQ ID NO: 1
29 <211> LENGTH: 468
30 <212> TYPE: DNA
31 <213> ORGANISM: Homo sapiens
33 <220> FEATURE:
34 <221> NAME/KEY: CDS
35 <222> LOCATION: (20)..(466)
36 <223> OTHER INFORMATION:
39 <220> FEATURE:
40 <221> NAME/KEY: mat_peptide
41 <222> LOCATION: (119)..()
42 <223> OTHER INFORMATION:
45 <220> FEATURE:
46 <221> NAME/KEY: misc_feature
47 <222> LOCATION: (301)..(301)
48 <223> OTHER INFORMATION: Unknown nucleotide.

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[illegible]

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```

65 Ile Lys Ala Ala Tyr Leu Ser Thr Ile Ser Lys Asp Leu Ile Thr Tyr
66          15          20          25
68 atg agt ggg acc aaa agt acc gag ttc aac aac acc gtc tct tgt agc      244
69 Met Ser Gly Thr Lys Ser Thr Glu Phe Asn Asn Thr Val Ser Cys Ser
70          30          35          40
72 aat cgg cca cat tgc ctt act gaa atc cag agc cta acc ttc aat ccc      292
73 Asn Arg Pro His Cys Leu Thr Glu Ile Gln Ser Leu Thr Phe Asn Pro
74          45          50          55
W--> 76 aac cgc cgn gtg cgg tcg ctc gcc aaa gaa atg ttc gcc atg aaa act      340
77 Asn Arg Arg Val Arg Ser Leu Ala Lys Glu Met Phe Ala Met Lys Thr
78          60          65          70
80 aag gct gcc tta gct atc tgg tgc cca ggc tat tcg gaa act cag ata      388
81 Lys Ala Ala Leu Ala Ile Trp Cys Pro Gly Tyr Ser Glu Thr Gln Ile
82 75          80          85          90
84 aat gct act cag gca atg aag aag agg aga aaa agg aaa gtc aca acc      436
85 Asn Ala Thr Gln Ala Met Lys Lys Arg Arg Lys Arg Lys Val Thr Thr
86          95          100          105
88 aat aaa tgt ctg gaa caa gtg tca caa tta aa      468
89 Asn Lys Cys Leu Glu Gln Val Ser Gln Leu
90          110          115
93 <210> SEQ ID NO: 2
94 <211> LENGTH: 149
95 <212> TYPE: PRT
96 <213> ORGANISM: Homo sapiens
98 <400> SEQUENCE: 2
100 Met Gly Cys Pro Arg Met Phe Pro Phe Ala Leu Leu Tyr Val Leu Ser
101          -30          -25          -20
104 Val Ser Phe Arg Lys Ile Phe Ile Leu Gln Leu Val Gly Leu Val Leu
105          -15          -10          -5
108 Thr Tyr Asp Phe Thr Asn Cys Asp Phe Glu Lys Ile Lys Ala Ala Tyr
109 -1 1          5          10          15
112 Leu Ser Thr Ile Ser Lys Asp Leu Ile Thr Tyr Met Ser Gly Thr Lys
113          20          25          30
116 Ser Thr Glu Phe Asn Asn Thr Val Ser Cys Ser Asn Arg Pro His Cys
117          35          40          45
120 Leu Thr Glu Ile Gln Ser Leu Thr Phe Asn Pro Asn Arg Arg Val Arg
121          50          55          60
124 Ser Leu Ala Lys Glu Met Phe Ala Met Lys Thr Lys Ala Ala Leu Ala
125          65          70          75
128 Ile Trp Cys Pro Gly Tyr Ser Glu Thr Gln Ile Asn Ala Thr Gln Ala
129 80          85          90          95

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132 <210> SEQ ID NO: 3

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133 <211> LENGTH: 149

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134 <212> TYPE: DNA

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135 <213> ORGANISM: Homo sapiens

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145 <220> FEATURE:
146 <221> NAME/KEY: CDS
147 <222> LOCATION: (1)..(477)
148 <223> OTHER INFORMATION:
151 <220> FEATURE:
152 <221> NAME/KEY: mat_peptide
153 <222> LOCATION: (85)..()
154 <223> OTHER INFORMATION:
157 <400> SEQUENCE: 3
158 atg ttc cct ttt gcc tta cta tat gtt ctg tca gtt tct ttc agg aaa      48
159 Met Phe Pro Phe Ala Leu Leu Tyr Val Leu Ser Val Ser Phe Arg Lys
160          -25          -20          -15
162 atc ttc atc tta caa ctt gta ggg ctg gtg tta act tac gac ttc act      96
163 Ile Phe Ile Leu Gln Leu Val Gly Leu Val Leu Thr Tyr Asp Phe Thr
164          -10          -5          -1  1
166 aac tgt gac ttt gag aag att aaa gca gcc tat ctc agt act att tct      144
167 Asn Cys Asp Phe Glu Lys Ile Lys Ala Ala Tyr Leu Ser Thr Ile Ser
168 5          10          15          20
170 aaa gac ctg att aca tat atg agt ggg acc aaa agt acc gag ttc aac      192
171 Lys Asp Leu Ile Thr Tyr Met Ser Gly Thr Lys Ser Thr Glu Phe Asn
172          25          30          35
174 aac acc gtc tct tgt agc aat cgg cca cat tgc ctt act gaa atc cag      240
175 Asn Thr Val Ser Cys Ser Asn Arg Pro His Cys Leu Thr Glu Ile Gln
176          40          45          50
178 agc cta acc ttc aat ccc acc gcc ggc tgc gcg tcg ctc gcc aaa gaa      288
179 Ser Leu Thr Phe Asn Pro Thr Ala Gly Cys Ala Ser Leu Ala Lys Glu
180          55          60          65
182 atg ttc gcc atg aaa act aag gct gcc tta gct atc tgg tgc cca gcc      336
183 Met Phe Ala Met Lys Thr Lys Ala Ala Leu Ala Ile Trp Cys Pro Gly
184          70          75          80
186 tat tcg gaa act caa ata aat gct act caa gca atg aag aag aag aag      384
187 Tyr Ser Glu Thr Gln Ile Asn Ala Thr Gln Ala Met Lys Lys Arg Arg
188 85          90          95          100
190 aaa aag aaa gtc aca acc aat aaa tgt ctg gaa caa gtc tca caa tta      432
191 Lys Arg Lys Val Thr Thr Asn Lys Cys Leu Glu Gln Val Ser Gln Leu
192          105          110          115
194 caa gga ttg tgg cgt cgc ttc aat cga cct tta ctg aaa caa cag taa      480
195 Gln Gly Leu Trp Arg Arg Phe Asn Arg Pro Leu Leu Lys Gln Gln
196          120          125          130
199 <210> SEQ ID NO: 4
200 <211> LENGTH: 159

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111 Ile Phe Ile Leu Gln Leu Val Gly Leu Val Leu Thr Tyr Asp Phe Thr
112          -10          -5          -1  1
114 aac tgt gac ttt gag aag att aaa gca gcc tat ctc agt act att tct

```

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215 5          10          15          20
218 Lys Asp Leu Ile Thr Tyr Met Ser Gly Thr Lys Ser Thr Glu Phe Asn
219          25          30          35
222 Asn Thr Val Ser Cys Ser Asn Arg Pro His Cys Leu Thr Glu Ile Gln
223          40          45          50
226 Ser Leu Thr Phe Asn Pro Thr Ala Gly Cys Ala Ser Leu Ala Lys Glu
227          55          60          65
230 Met Phe Ala Met Lys Thr Lys Ala Ala Leu Ala Ile Trp Cys Pro Gly
231          70          75          80
234 Tyr Ser Glu Thr Gln Ile Asn Ala Thr Gln Ala Met Lys Lys Arg Arg
235 85          90          95          100
238 Lys Arg Lys Val Thr Thr Asn Lys Cys Leu Glu Gln Val Ser Gln Leu
239          105          110          115
242 Gln Gly Leu Trp Arg Arg Phe Asn Arg Pro Leu Leu Lys Gln Gln
243          120          125          130
246 <210> SEQ ID NO: 5
247 <211> LENGTH: 176
248 <212> TYPE: PRT
249 <213> ORGANISM: ovine
251 <400> SEQUENCE: 5
253 Met Phe His Val Ser Phe Arg Tyr Ile Phe Gly Ile Pro Pro Leu Ile
254 1          5          10          15
257 Leu Val Leu Leu Pro Val Ala Ser Ser Asp Cys Asp Phe Ser Gly Lys
258          20          25          30
261 Asp Gly Gly Ala Tyr Gln Asn Val Leu Met Val Ser Ile Asp Asp Leu
262          35          40          45
265 Asp Asn Met Ile Asn Phe Asp Ser Asn Cys Leu Asn Asn Glu Pro Asn
266          50          55          60
269 Phe Phe Lys Lys His Ser Cys Asp Asp Asn Lys Glu Ala Ser Phe Leu
270 65          70          75          80
273 Asn Arg Ala Ala Arg Lys Leu Lys Gln Phe Leu Lys Met Asn Ile Ser
274          85          90          95
277 Asp Asp Phe Lys Leu His Leu Ser Thr Val Ser Gln Gly Thr Leu Thr
278          100          105          110
281 Leu Leu Asn Cys Thr Ser Lys Gly Lys Gly Arg Lys Pro Pro Ser Leu
282          115          120          125
285 Gly Glu Ala Gln Pro Thr Lys Asn Leu Glu Glu Asn Lys Ser Leu Lys
286          130          135          140
289 Glu Gln Arg Lys Gln Asn Asp Leu Cys Phe Leu Lys Ile Leu Leu Gln
290 145          150          155          160
293 Lys Ile Lys Thr Cys Trp Asn Lys Ile Leu Arg Gly Ile Thr Glu His
          165          170          175

```

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294 Met Phe His Val Ser Phe Arg Tyr Ile Phe Gly Ile Pro Pro Leu Ile
          10          15

```

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302 <400> SEQUENCE: 5

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304 Met Phe His Val Ser Phe Arg Tyr Ile Phe Gly Ile Pro Pro Leu Ile
          10          15

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```

308 Leu Val Leu Leu Pro Val Ala Ser Ser Asp Cys Asp Ile Ser Gly Lys
309                20                25                30
312 Asp Gly Gly Ala Tyr Gln Asn Val Leu Met Val Asn Ile Asp Asp Leu
313                35                40                45
316 Asp Asn Met Ile Asn Phe Asp Ser Asn Cys Leu Asn Asn Glu Pro Asn
317                50                55                60
320 Phe Phe Lys Lys His Ser Cys Asp Asp Asn Lys Glu Ala Ser Phe Leu
321 65                70                75                80
324 Asn Arg Ala Ser Arg Lys Leu Arg Gln Phe Leu Lys Met Asn Ile Ser
325                85                90                95
328 Asp Asp Phe Lys Leu His Leu Ser Thr Val Ser Gln Gly Thr Leu Thr
329                100               105               110
332 Leu Leu Asn Cys Thr Ser Lys Gly Lys Gly Arg Lys Pro Pro Ser Leu
333                115               120               125
336 Ser Glu Ala Gln Pro Thr Lys Asn Leu Glu Glu Asn Lys Ser Ser Lys
337                130               135               140
340 Glu Gln Lys Lys Gln Asn Asp Leu Cys Phe Leu Lys Ile Leu Leu Gln
341 145                150               155               160
344 Lys Ile Lys Thr Cys Trp Asn Lys Ile Leu Arg Gly Ile Lys Glu His
345                165               170               175

```

348 <210> SEQ ID NO: 7

349 <211> LENGTH: 177

350 <212> TYPE: PRT

351 <213> ORGANISM: Homo sapiens

353 <400> SEQUENCE: 7

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355 Met Phe His Val Ser Phe Arg Tyr Ile Phe Gly Leu Pro Pro Leu Ile
356 1                5                10                15
359 Leu Val Leu Leu Pro Val Ala Ser Ser Asp Cys Asp Ile Glu Gly Lys
360                20                25                30
363 Asp Gly Lys Gln Tyr Glu Ser Val Leu Met Val Ser Ile Asp Gln Leu
364                35                40                45
367 Leu Asp Ser Met Lys Glu Ile Gly Ser Asn Cys Leu Asn Asn Glu Phe
368                50                55                60
371 Asn Phe Phe Lys Arg His Ile Cys Asp Ala Asn Lys Glu Gly Met Phe
372 65                70                75                80
375 Leu Phe Arg Ala Ala Arg Lys Leu Arg Gln Phe Leu Lys Met Asn Ser
376                85                90                95
379 Thr Gly Asp Phe Asp Leu His Leu Leu Lys Val Ser Glu Gly Thr Thr
380                100               105               110
383 Ile Leu Leu Asn Cys Thr Gly Gln Val Lys Gly Arg Lys Pro Ala Ala
384                115               120               125

```

387 Leu Val Leu Leu Pro Val Ala Ser Ser Asp Cys Asp Ile Ser Gly Lys

388 130 135 140

389 His

RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/09/963,347B

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Input Set : A:\DX0903K1.ST25.txt
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; N Pos. 301

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/963,347B

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Input Set : A:\DX0903K1.ST25.txt

Output Set: N:\CRF4\09272002\I963347B.raw

L:76 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:292